In the Specification;

On page 1 of the specification, please amend the Related Applications paragraph as follows:

This application is a divisional application of U.S. Patent Application Serial No. 09/439,165 filed on November 12, 1999, now abandoned, which is a continuation-in-part application of U.S. Patent Application Serial No. 09/421,134 filed on October 19, 1999, now abandoned, which is a continuation-in-part application of U.S. Patent Application Serial No. 09/258,633 filed February 26, 1999, now abandoned, which claims the benefit of U.S. Provisional Patent Application Serial No. 60/114,078 filed December 28, 1998 and of U.S. Provisional Patent Application Serial No. 60/108,322 filed November 13, 1998, all of which are ~~claims priority to U.S. provisional Application No. 60/108,322, filed on November 13, 1998, U.S. provisional Application No. 60/114,078 filed on December 28, 1998, U.S. Patent Application Serial No.: 09/258,633 filed on February 26, 1999, and U.S. Patent Application Serial No.: 09/421,134 filed on October 19, 1999,~~ incorporated herein in their entirety by this reference.

On page 6, please replace the paragraph beginning on line 35 with the following:

Figures 1A-1D depict ~~Figure 1 depicts~~ the full length cDNA sequence and predicted amino acid sequence of human VR-1 (hVR-1). The nucleotide sequence corresponds to nucleic acids 1 to 3909 of SEQ ID NO:1. The amino acid sequence corresponds to amino acids 1 to 839 of SEQ ID NO:2. The coding region without the 5' and 3' untranslated regions of the human VR-1 (hVR-1) gene is shown in SEQ ID NO:3.

On page 7, please replace the paragraph beginning on line 3 with the following:

Figures 2A-2C depict ~~Figure 2 depicts~~ the full length cDNA sequence and predicted amino acid sequence of human VR-2 (hVR-2). The nucleotide sequence corresponds to nucleic acids 1 to 2809 of SEQ ID NO:4. The amino acid sequence corresponds to amino acids 1 to 764 of SEQ ID NO:5. The coding region without the 5' and 3' untranslated regions of the human VR-2 (hVR-2) gene is shown in SEQ ID NO:6.

On page 7, please replace the paragraph beginning on line 8 with the following:

Figures 3A-3B depict ~~Figure 3 depicts~~ the partial cDNA sequence and partial predicted amino acid sequence of an alternate form of human VR-2 (hVR-2). The nucleotide sequence corresponds to nucleic acids 1 to 1489 of SEQ ID NO:7. The amino acid sequence corresponds to amino acids 1 to 436 of SEQ ID NO:8. The coding region without the 5' and 3' untranslated regions of the alternate form of human VR-2 (hVR-2) gene is shown in SEQ ID NO:9.

On page 7, please replace the paragraph beginning on line 13 with the following:

Figures 4A-4B depict ~~Figure 4 depicts~~ the partial cDNA sequence and partial predicted amino acid sequence of rat VR-2 (rVR-2). The nucleotide sequence corresponds to nucleic acids 1 to 1794 of SEQ ID NO:10. The amino acid sequence corresponds to amino acids 1 to 554 of SEQ ID NO:11. The coding region without the 5' and 3' untranslated regions of the rat VR-2 (rVR-2) gene is shown in SEQ ID NO:12.

On page 7, please replace the paragraph beginning on line 18 with the following:

Figures 5A-5B depict ~~Figure 5 depicts~~ an alignment of the hVR-1 protein (SEQ ID NO:2) with the human VR-2 protein (SEQ ID NO:5) using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4.

On page 7, please replace the paragraph beginning on line 21 with the following:

Figures 6A-6F depict ~~Figure 6 depicts~~ an alignment of the hVR-1 nucleotide sequence (SEQ ID NO:1) with the human VR-2 nucleotide sequence (SEQ ID NO:4) using the GAP program in the GCG software package (nwsgapdna matrix) and a gap weight of 50 and a length weight of 3.

On page 7, please replace the paragraph beginning on line 26 with the following:

Figures 8A-8B depict ~~Figure 8 depicts~~ an alignment of the hVR-2 protein (SEQ ID NO:5) with the rat VR-2 protein (SEQ ID NO:11) using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4.

On page 7, please replace the paragraph beginning on line 29 with the following:

Figures 9A-9F depict ~~Figure 9 depicts~~ an alignment of the hVR-1 nucleotide sequence (SEQ ID NO:1) with the rat VR-1 nucleotide sequence (Accession Number:AF029310 (SEQ ID NO:21) using the GAP program in the GCG software package (nwsgapdna matrix) and a gap weight of 50 and a length weight of 3.

On page 7, please replace the paragraph beginning on line 32 with the following:

Figures 10A-10B depict ~~Figure 10 depicts~~ an alignment of the hVR-1 protein (SEQ ID NO:2) with the rat VR-1 protein (Accession Number:AF029310 (SEQ ID NO:22) using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4.

On page 8, please replace the paragraph beginning on line 3 with the following:

Figure 13 depicts an alignment between the amino acid sequence of the hVR-1 protein (SEQ ID NO:2) and Ank repeat domains (SEQ ID NO:23) identified while performing ~~the results~~ of a search using the amino acid sequence of the hVR-1 protein against the HMM database.

On page 8, please replace the paragraph beginning on line 7 with the following:

Figure 15 depicts an alignment between the amino acid sequence of the hVR-2 protein (SEQ ID NO:5) and Ank repeat domains (SEQ ID NO:23) identified while performing ~~the results~~ of a search using the amino acid sequence of the hVR-2 protein against the HMM database.

On page 12, please replace the paragraph beginning on line 14 with the following:

The nucleotide sequence of the full length hVR-1 cDNA and the predicted amino acid sequence of the hVR-1 polypeptide are shown in Figures 1A-1D ~~Figure 1~~ and in SEQ ID NOs:1 and 2, respectively.

On page 12, please replace the paragraph beginning on line 17 with the following:

The nucleotide sequence of the full length hVR-2 cDNA and the predicted amino acid sequence of the hVR-2 polypeptide are shown in <u>Figures 2A-2B</u> ~~Figure 2~~ and in SEQ ID NOs:4 and 5, respectively.

On page 12, please replace the paragraph beginning on line 20 with the following:

The nucleotide sequence of the partial hVR-2 (alternate form) cDNA and the predicted amino acid sequence of the hVR-2 (alternate form) polypeptide are shown in <u>Figures 3A-3B</u> ~~Figure 3~~ and in SEQ ID NOs:7 and 8, respectively.

On page 12, please replace the paragraph beginning on line 23 with the following:

The nucleotide sequence of the partial rVR-2 cDNA and the predicted amino acid sequence of the rVR-2 polypeptide are shown in <u>Figures 4A-4B</u> ~~Figure 4~~ and in SEQ ID NOs:10 and 11, respectively.

On page 65, please replace the paragraph beginning on line 26 with the following:

The nucleotide sequence of the full length hVR-1 cDNA and the predicted amino acid sequence of the hVR-1 polypeptide are shown in <u>Figures 1A-1D</u> ~~Figure 1~~ and in SEQ ID NOs:1 and 2, respectively.

On page 65, please replace the paragraph beginning on line 29 with the following:

The nucleotide sequence of the full length hVR-2 cDNA and the predicted amino acid sequence of the hVR-2 polypeptide are shown in <u>Figures 2A-2B</u> ~~Figure 2~~ and in SEQ ID NOs:4 and 5, respectively.

On page 65, please replace the paragraph beginning on line 32 with the following:

The nucleotide sequence of the partial hVR-2 (alternate form) cDNA and the predicted amino acid sequence of the hVR-2 (alternate form) polypeptide are shown in <u>Figures 3A-3B</u> ~~Figure 3~~ and in SEQ ID NOs:7 and 8, respectively.

On page 65, please replace the paragraph beginning on line 37 with the following:

The nucleotide sequence of the partial rVR-2 cDNA and the predicted amino acid sequence of the rVR-2 polypeptide are shown in Figures 4A-4B ~~Figure 4~~ and in SEQ ID NOs:10 and 11, respectively.

On page 66, please replace the paragraph beginning on line 1 with the following:

The hVR-1 protein (SEQ ID NO:2) was aligned with the human VR-2 protein (SEQ ID NO:5) using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4. The results showed a 46.348% identity and 55.378% similarity between the two sequences (see Figures 5A-5B ~~Figure 5~~).

On page 66, please replace the paragraph beginning on line 7 with the following:

The hVR-1 nucleotide sequence (SEQ ID NO:1) was aligned with the human VR-2 nucleotide sequence (SEQ ID NO:4) using the GAP program in the GCG software package (nwsgapdna matrix) and a gap weight of 50 and a length weight of 3. The results showed a 55.316% identity and 55.316% similarity between the two sequences (see Figures 6A-6F ~~Figure 6~~).

On page 66, please replace the paragraph beginning on line 11 with the following:

The hVR-2 protein (SEQ ID NO:5) was aligned with the rat VR-2 protein (SEQ ID NO:11) using the CLUSTAL W (1.74) multiple sequence alignment program (Figure 7), as well as using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4. The results showed a 79.167% identity and 81.703% similarity between the two sequences (see Figures 8A-8B ~~Figure 8~~).

On page 66, please replace the paragraph beginning on line 16 with the following:

The hVR-1 nucleotide sequence (SEQ ID NO:1) was aligned with the rat VR-1 nucleotide sequence (Accession Number:AF029310 (SEQ ID NO:21)) using the GAP program in the GCG software package (nwsgapdna matrix) and a gap weight of 50 and a length weight of 3.

The results showed a 82.125% identity and 82.125% similarity between the two sequences (see Figures 9A-9F ~~Figure 9~~).

On page 66, please replace the paragraph beginning on line 20 with the following:

The hVR-1 protein (SEQ ID NO:2) was aligned with the rat VR-1 protein (Accession Number:AF029310 (SEQ ID NO:22)) using the GAP program in the GCG software package (Blosum 62 matrix) and a gap weight of 12 and a length weight of 4. The results showed a 86.022% identity and 89.247% similarity between the two sequences (see Figures 10A-10B ~~Figure 10~~).